SEQUENCE LISTING

<110> University of British Columbia, et al.

<120> CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS

<130> 80021-255

<140> US 09/835,107
<141> 2001-04-12

<150> CA 2,305,036
<151> 2000-04-12

<150> US 60/232,425
<151> 2000-09-14

<150> CA 2,335,109
<151> 2001-02-23

<160> 31

<170> PatentIn Ver. 2.0

<210> 1
<211> 67
<212> PRT
<213> Homo sapiens

<220>
<223> SDF-1 alpha

<220>
<221> MISC_FEATURE
<222> (1)..(67)
<223> A pegylation moiety may be provided at any position on the sequence.

<400> 1
Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro Cys Arg Phe Phe Glu Ser
1   5   10   15

His Val Ala Arg Ala Asn Val Lys His Leu Lys Ile Leu Asn Thr Pro
            20   25   30

Asn Cys Ala Leu Gln Ile Val Ala Arg Leu Lys Asn Asn Asn Arg Gln
        35   40   45

Val Cys Ile Asp Pro Lys Leu Lys Trp Ile Gln Glu Tyr Leu Glu Lys
    50   55   60

Ala Leu Asn
65

<210> 2
<211> 93
<212> PRT
<213> Homo sapiens

<220>

<223> SDF-1 Precursor, PBSF

<220>
<221>   MISC_FEATURE
<222>   (1)..(93)
<223>   A pegylation moiety may be provided at any position on the
         sequence.

<400> 2

```
Met Asn Ala Lys Val Val Val Val Leu Val Leu Val Leu Thr Ala Leu
 1           5              10              15
Cys Leu Ser Asp Gly Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro Cys
             20              25              30
Arg Phe Phe Glu Ser His Val Ala Arg Ala Asn Val Lys His Leu Lys
         35              40              45
Ile Leu Asn Thr Pro Asn Cys Ala Leu Gln Ile Val Ala Arg Leu Lys
     50              55              60
Asn Asn Asn Arg Gln Val Cys Ile Asp Pro Lys Leu Lys Trp Ile Gln
 65              70              75              80
Glu Tyr Leu Glu Lys Ala Leu Asn Lys Arg Phe Lys Met
             85              90
```

<210> 3
<211> 93
<212> PRT
<213> Homo sapiens

<220>
<223> SDF-1 beta

<220>
<221>   MISC_FEATURE
<222>   (1)..(93)
<223>   A pegylation moiety may be provided at any position on the
         sequence.

<400> 3

```
Met Asn Ala Lys Val Val Val Val Leu Val Leu Val Leu Thr Ala Leu
 1           5              10              15
Cys Leu Ser Asp Gly Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro Cys
             20              25              30
Arg Phe Phe Glu Ser His Val Ala Arg Ala Asn Val Lys His Leu Lys
         35              40              45
Ile Leu Asn Thr Pro Asn Cys Ala Leu Gln Ile Val Ala Arg Leu Lys
     50              55              60
Asn Asn Asn Arg Gln Val Cys Ile Asp Pro Lys Leu Lys Trp Ile Gln
 65              70              75              80
Glu Tyr Leu Glu Lys Ala Leu Asn Lys Arg Phe Lys Met
             85              90
```

2

```
<210> 4
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesised in Laboratory: SDF-1(1-17): or
      CTCE9902

<400> 4
Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro Cys Arg Phe Phe Glu Ser
 1               5                   10                  15

His


<210> 5
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesised in Laboratory

<400> 5
Arg Phe Phe Glu Ser His
 1               5


<210> 6
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesised in Laboratory

<400> 6
Lys Pro Val Ser Leu Ser Tyr Arg Cys
 1               5


<210> 7
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> DISULFID
<222> (9)
<223> Disulphide linkage may form between two cys
      residues at position 9 of each of two monomers
      thereby forming a dimer.

<220>
<223> Synthesised in Laboratory:
      SDF-1(1-9)2-C9/C9-cysteine dimer: or CTCE9901
```

<400> 7
Lys Pro Val Ser Leu Ser Tyr Arg Cys
   1   5

<210> 8
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesised in Laboratory

<220>
<221> BINDING
<222> (9)
<223> Linking Moiety (may be lysine with both the alpha and the
      epsilon amino groups of the lysine being associated with
      the covalent (amide) bond formation) may bind here allowing
      formation of a dimer.

<400> 8
Lys Pro Val Ser Leu Ser Tyr Arg Cys
   1   5

<210> 9
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesised in Laboratory

<220>
<221> BINDING
<222> (8)
<223> Linking Moiety (may be lysine with both the alpha and the
      epsilon amino groups of the lysine being associated with
      the covalent (amide) bond formation) may bind here allowing
      formation of a dimer.

<400> 9
Lys Pro Val Ser Leu Ser Tyr Arg
   1   5

<210> 10
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<221> DOMAIN
<222> (15)..(17)
<223> spacer monomers (such as the illustrated glycine
      G's) may be used in variable numbers, such as 2, 3
      or 4 glycines.

<220>
<223> Synthesised in Laboratory:

4

SDF-1(1-14)-(G)3-SDF-1(55-67) acid

<400> 10
Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro Cys Arg Phe Phe Gly Gly
1   5   10   15

Gly Leu Lys Trp Ile Gln Glu Tyr Leu Glu Lys Ala Leu Asn
        20   25   30

<210> 11
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
<221> DOMAIN
<222> (16)..(19)
<223> spacer monomers (such as the illustrated glycine
      G's) may be used in variable numbers, such as 2, 3
      or 4 glycines.

<220>
<223> Synthesised in Laboratory:
      SDF-1(1-14)-(G)4-SDF-1(55-67) acid: or CTCE0013

<400> 11
Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro Cys Arg Phe Phe Gly Gly
1   5   10   15

Gly Gly Leu Lys Trp Ile Gln Glu Tyr Leu Glu Lys Ala Leu Asn
            20   25   30

<210> 12
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<221> DOMAIN
<222> (15)..(17)
<223> spacer monomers (such as the illustrated glycine
      G's) may be used in variable numbers, such as 2, 3
      or 4 glycines.

<220>
<223> Synthesised in Laboratory:
      SDF-1(1-14)-(G)3-SDF-1(55-67) amide

<220>
<221> MOD_RES
<222> (30)
<223> AMIDATION

<400> 12
Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro Cys Arg Phe Phe Gly Gly
1   5   10   15

Gly Leu Lys Trp Ile Gln Glu Tyr Leu Glu Lys Ala Leu Asn
        20   25   30

<210> 13
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
<221> DOMAIN
<222> (15)..(18)
<223> spacer monomers (such as the illustrated glycine
      G's) may be used in variable numbers, such as 2, 3
      or 4 glycines.

<220>
<223> Synthesised in Laboratory:
      SDF-1(1-14)-(G)4-SDF-1(55-67) amide: or CTCE0017

<220>
<221> MOD_RES
<222> (31)
<223> AMIDATION

<400> 13
Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro Cys Arg Phe Phe Gly Gly
 1   5   10   15

Gly Gly Leu Lys Trp Ile Gln Glu Tyr Leu Glu Lys Ala Leu Asn
            20   25   30

<210> 14
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<221> DOMAIN
<222> (18)..(21)
<223> spacer monomers (such as the illustrated glycine
      G's) may be used in variable numbers, such as 2, 3
      or 4 glycines.

<220>
<223> Synthesised in Laboratory:
      SDF-1(1-17)-(G)3-SDF-1(55-67) acid

<400> 14
Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro Cys Arg Phe Phe Glu Ser
 1   5   10   15

His Gly Gly Gly Leu Lys Trp Ile Gln Glu Tyr Leu Glu Lys Ala Leu
            20   25   30

Asn

<210> 15
<211> 34
<212> PRT

<213> Artificial Sequence

<220>
<221> DOMAIN
<222> (18)..(21)
<223> spacer monomers (such as the illustrated glycine
      G's) may be used in variable numbers, such as 2, 3
      or 4 glycines.

<220>
<223> Synthesised in Laboratory:
      SDF-1(1-17)-(G)4-SDF-1(55-67) acid

<400> 15
Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro Cys Arg Phe Phe Glu Ser
 1   5   10   15

His Gly Gly Gly Gly Leu Lys Trp Ile Gln Glu Tyr Leu Glu Lys Ala
             20   25   30

Leu Asn

<210> 16
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<221> DOMAIN
<222> (18)..(20)
<223> spacer monomers (such as the illustrated glycine
      G's) may be used in variable numbers, such as 2, 3
      or 4 glycines.

<220>
<223> Synthesised in Laboratory:
      SDF-1(1-17)-(G)3-SDF-1(55-67) amide

<220>
<221> MOD_RES
<222> (33)
<223> AMIDATION

<400> 16
Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro Cys Arg Phe Phe Glu Ser
 1   5   10   15

His Gly Gly Gly Leu Lys Trp Ile Gln Glu Tyr Leu Glu Lys Ala Leu
             20   25   30

Asn

<210> 17
<211> 34
<212> PRT
<213> Artificial Sequence

```
<220>
<221> DOMAIN
<222> (18)..(21)
<223> spacer monomers (such as the illustrated glycine
      G's) may be used in variable numbers, such as 2, 3
      or 4 glycines.


<220>
<223> Synthesised in Laboratory:
      SDF-1(1-17)-(G)3-SDF-1(55-67) amide


<220>
<221> MOD_RES
<222> (34)
<223> AMIDATION


<400> 17
Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro Cys Arg Phe Phe Glu Ser
 1               5              10             15


His Gly Gly Gly Gly Leu Lys Trp Ile Gln Glu Tyr Leu Glu Lys Ala
             20              25              30


Leu Asn




<210> 18
<211> 31
<212> PRT
<213> Artificial Sequence


<220>
<221> DOMAIN
<222> (15)..(18)
<223> spacer monomers (such as the illustrated glycine
      G's) may be used in variable numbers, such as 2, 3
      or 4 glycines.


<220>
<221> DOMAIN
<222> (24)..(28)
<223> Cyclized, for example glutamate (E) and lysine (K)
      residues may be joined by side chain cyclization
      using a lactam formation procedure.


<220>
<223> Synthesised in Laboratory:
      SDF-1(1-14)-(G)4-SDF(55-67)-E24/K28-cyclic acid


<400> 18
Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro Cys Arg Phe Phe Gly Gly
 1               5              10             15


Gly Gly Leu Lys Trp Ile Gln Glu Tyr Leu Glu Lys Ala Leu Asn
             20              25              30



<210> 19
<211> 31
<212> PRT
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8

<213> Artificial Sequence

<220>
<221> DOMAIN
<222> (15)..(18)
<223> spacer monomers (such as the illustrated glycine
      G's) may be used in variable numbers, such as 2, 3
      or 4 glycines.

<220>
<221> DOMAIN
<222> (20)..(24)
<223> Cyclized, for example glutamate (E) and lysine (K)
      residues may be joined by side chain cyclization
      using a lactam formation.

<220>
<223> Synthesised in Laboratory:
      SDF-1(1-14)-(G)4-SDF-1(55-67)-K20/E24-cyclic acid

<400> 19
Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro Cys Arg Phe Phe Gly Gly
1   5   10   15

Gly Gly Leu Lys Trp Ile Gln Glu Tyr Leu Glu Lys Ala Leu Asn
            20   25   30

<210> 20
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
<221> DOMAIN
<222> (15)..(18)
<223> spacer monomers (such as the illustrated glycine
      G's) may be used in variable numbers, such as 2, 3
      or 4 glycines.

<220>
<221> DOMAIN
<222> (24)..(28)
<223> Cyclized, for example (E) and lysine (K) residues
      may be joined by side chain cyclization using a
      lactam formation procedure.

<220>
<223> Synthesised in Laboratory:
      SDF-1(1-14)-(G)4-SDF-1(55-67)-E24/K28-cyclic
      amide: or CTCE0022

<220>
<221> MOD_RES
<222> (31)
<223> AMIDATION

<400> 20
Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro Cys Arg Phe Phe Gly Gly
1   5   10   15

```
Gly Gly Leu Lys Trp Ile Gln Glu Tyr Leu Glu Lys Ala Leu Asn
         20                      25                   30
```

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<210> 21
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
<221> DOMAIN
<222> (15)..(18)
<223> spacer monomers (such as the illustrated glycine
      G's) may be used in variable numbers, such as 2, 3
      or 4 glycines.


<220>
<221> DOMAIN
<222> (20)..(24)
<223> Clyclized, for example glutamate (E) and lysine
      (K) residues may be joined by side chain
      cyclization using a lactam formation procedure.


<220>
<223> Synthesised in Laboratory:
      SDF-1(1-14)-(G)4-SDF-1(55-67)-K20/E24-cyclic
      amide: or CTCE0021


<220>
<221> MOD_RES
<222> (31)
<223> AMIDATION

<400> 21
Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro Cys Arg Phe Phe Gly Gly
  1               5               10                   15

Gly Gly Leu Lys Trp Ile Gln Glu Tyr Leu Glu Lys Ala Leu Asn
         20                      25                   30


<210> 22
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
<221> DOMAIN
<222> (15)..(18)
<223> spacer monomers (such as the illustrated glycine
      G's) may be used in variable numbers, such as 2, 3
      or 4 glycines.


<220>
<221> DOMAIN
<222> (20)..(24)
<223> Internal cyclization of peptides of the invention
      may be in alternative positions, or between
      substituted amino acids.  The nature of the cyclic
      linkage may also be varied.
```

<220>
<223> Synthesised in Laboratory:
      SDF-1(1-14)-(G)4)-SDF-1(55-67)-K20/D24-cyclic acid

<400> 22
Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro Cys Arg Phe Phe Gly Gly
 1   5   10   15

Gly Gly Leu Lys Trp Ile Gln Asp Tyr Leu Glu Lys Ala Leu Asn
            20   25   30

<210> 23
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
<221> DOMAIN
<222> (15)..(18)
<223> spacer monomers (such as the illustrated glycine
      G's) may be used in variable numbers, such as 2, 3
      or 4 glycines.

<220>
<221> DOMAIN
<222> (20)..(24)
<223> Internal cyclization of peptides of the invention
      may be in alternative positions, or between
      substituted amino acids. The nature of the cyclic
      linkage may also be varied.

<220>
<223> Synthesised in Laboratory:
      SDF-1(1-14)-(G)4-SDF-1(55-67)-K20/D24-cyclic amide

<220>
<221> MOD_RES
<222> (31)
<223> AMIDATION

<400> 23
Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro Cys Arg Phe Phe Gly Gly
 1   5   10   15

Gly Gly Leu Lys Trp Ile Gln Asp Tyr Leu Glu Lys Ala Leu Asn
            20   25   30

<210> 24
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
<221> DOMAIN
<222> (15)..(18)
<223> spacer monomers (such as the illustrated glycine
      G's) may be used in variable numbers, such as 2, 3
      or 4 glycines.

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<220>
<221> DISULFID
<222> (9)..(11)
<223> cystein residues may for example be involved in
      bridge formation


<220>
<223> Synthesised in Laboratory:
      SDF-1(1-14)-(G)4-SDF-1(55-67)-C9/C11-cyclic acid


<400> 24
Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro Cys Arg Phe Phe Gly Gly
 1               5               10              15

Gly Gly Leu Lys Trp Ile Gln Glu Tyr Leu Glu Lys Ala Leu Asn
          20              25              30



<210> 25
<211> 31
<212> PRT
<213> Artificial Sequence


<220>
<221> DOMAIN
<222> (15)..(18)
<223> spacer monomers (such as the illustrated glycine
      G's) may be used in variable numbers, such as 2, 3
      or 4 glycines.


<220>
<221> DISULFID
<222> (9)..(11)
<223> Cysteine residues may for example be invloved in
      bridge formation.


<220>
<223> Synthesised in Laboratory:
      SDF-1(1-14)-(G)4-SDF-1(55-67)-C9/C11-cyclic amide


<220>
<221> MOD_RES
<222> (31)
<223> AMIDATION


<400> 25
Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro Cys Arg Phe Phe Gly Gly
 1               5               10              15

Gly Gly Leu Lys Trp Ile Gln Glu Tyr Leu Glu Lys Ala Leu Asn
          20              25              30



<210> 26
<211> 33
<212> PRT
<213> Artificial Sequence


<220>
<223> Synthesised in Laboratory: SDF-1(1-14)-(G)4-MIP-1
      alpha(36-50)acid or amide.
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<220>
<221> MOD_RES
<222> (33)
<223> Possible Amidation

<400> 26
Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro Cys Arg Phe Phe Gly Gly
 1               5                  10                  15

Gly Gly Ser Lys Pro Gly Val Ile Phe Leu Thr Lys Arg Ser Arg Gln
            20              25                  30

Val


<210> 27
<211> 58
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesised in Laboratory: SDF-1(1-14)-(G)4-MIP-1
      alpha(11-50)-acid or amide

<220>
<221> MOD_RES
<222> (58)
<223> Possible Amidation

<400> 27
Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro Cys Arg Phe Phe Gly Gly
 1               5                  10                  15

Gly Gly Cys Cys Phe Ser Tyr Thr Ser Arg Gln Ile Pro Gln Asn Phe
            20              25                  30

Ile Ala Asp Tyr Phe Glu Thr Ser Ser Gln Cys Ser Lys Pro Gly Val
        35              40                  45

Ile Phe Leu Thr Lys Arg Ser Arg Gln Val
    50              55


<210> 28
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesised in Laboratory: SDF-1(1-14)-(G)4-MIP-1
      alpha(56-70)-acid or amide

<220>
<221> MOD_RES
<222> (33)
<223> Possible Amidation
```

<400> 28
Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro Cys Arg Phe Phe Gly Gly
1   5   10   15

Gly Gly Glu Glu Trp Val Gln Lys Tyr Val Asp Asp Leu Glu Leu Ser
            20   25   30

Ala

<210> 29
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> BINDING
<222> (9)
<223> Lysine bridge may or may not be present between each of two arg
      residues at position 8 of each of two monomers thereby forming a dimer.

<220>
<223> Synthesised in Laboratory: SDF-1(1-8)2-lysine
      bridge dimer: or CTCE9904

<220>
<221> MOD_RES
<222> (9)
<223> AMIDATION

<400> 29
Lys Pro Val Ser Leu Ser Tyr Arg Lys
1   5

<210> 30
<211> 40
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesised in Laboratory

<400> 30
Cys Cys Phe Ser Tyr Thr Ser Arg Gln Ile Pro Gln Asn Phe Ile Ala Asp Tyr Phe
1   5   10   15

Glu Thr Ser Ser Gln Cys Ser Lys Pro Gly Val Ile Phe Leu Thr Lys Arg
20   25   30   35

Ser Arg Gln Val
            40

<210> 31
<211> 33
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthesised in Laboratory: SDF-1(1-14)-(G)4-MIP-1
      alpha(36-50)-acid

<400> 31
Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro Cys Arg Phe Phe Gly Gly
  1   5   10   15

Gly Gly Ser Lys Pro Gly Val Ile Phe Leu Thr Lys Arg Ser Arg Gln
            20   25   30

Val